



## RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 16 USC, 216.A  
Source: CIPE  
Date Processed by STIC: 6/28/02

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

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<http://www.uspto.gov/web/offices/pac/checker>

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
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4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



Does Not Comply  
Corrected Diskette Needed

OIPE

## RAW SEQUENCE LISTING

DATE: 06/28/2002

PATENT APPLICATION: US/10/050,216A

TIME: 11:16:21

Input Set : A:\CORRECTEDSEQUENCE LISTING.txt

Output Set: N:\CRF3\06282002\J050216A.raw

4 <110> APPLICANT: Curtis, Rory A.J., Lora, Jose M.  
6 <120> TITLE OF INVENTION: 46798: A Human Matrix Metalloprotease and  
7 Uses Therefore  
9 <130> FILE REFERENCE: MPI2001-014P1RNM  
11 <140> CURRENT APPLICATION NUMBER: 10/050,216A  
C--> 13 <141> CURRENT FILING DATE: 2002-01-16  
15 <150> PRIOR APPLICATION NUMBER: 60/262,252  
17 <151> PRIOR FILING DATE: 2001-01-16  
19 <160> NUMBER OF SEQ ID NOS: 10  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## ERRORED SEQUENCES

746 <210> SEQ ID NO: 10  
747 <211> LENGTH: 1560 *found 1563!*  
748 <212> TYPE: DNA  
749 <213> ORGANISM: Homo sapiens  
751 <220> FEATURE:  
752 <221> NAME/KEY: CDS  
753 <222> LOCATION: (1)...(1560)  
755 <400> SEQUENCE: 10  
756 atg gtc gcg cgc gtc ggc etc ctg ctg cgc gcc ctg cag ctg cta ctg 48  
757 Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu  
758 1 5 10 15  
760 tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg 96  
761 Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu  
762 20 25 30  
764 cgc aag gag gcg gag gca ttc cta gag aag tac gga tac etc aat gaa 144  
765 Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu  
766 35 40 45  
768 cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga 192  
769 Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg  
770 50 55 60  
772 gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc 240  
773 Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg  
774 65 70 75 80  
776 gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc 288  
777 Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr  
778 85 90 95  
780 aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga 336  
781 Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg  
782 100 105 110

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784 cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggt aac 384
785 His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Asn
786      115      120      125
788 aaa tgg tac aag cag cac ctc tcc tac cgc ctg gtg aac tgg cct gag 432
789 Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu
790      130      135      140
792 cat ctg ccg gag ccg gca gtt cgg ggc gcc gtg cgc gcc gcc ttc cag 480
793 His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln
794 145      150      155      160
796 ttg tgg agc aac gtc tca gcg ctg gag ttc tgg gag gcc cca gcc aca 528
797 Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr
798      165      170      175
800 ggc ccc gct gac atc cgg ctc acc ttc ttc caa ggg gac cac aac gat 576
801 Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp
802      180      185      190
804 ggg ctg ggc aat gcc ttt gat ggc cca ggg ggc gcc ctg gcg cac gcc 624
805 Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala
806      195      200      205
808 ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac caa gat gag cgc tgg 672
809 Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp
810      210      215      220
812 tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc gtg gtg ctg gcg cac 720
813 Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe Val Val Leu Ala His
814 225      230      235      240
816 gag atc ggt cac acg ctt ggc ctc acc cac tcg ccc gcg ccg cgc gcg 768
817 Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala
818      245      250      255
820 ctc atg gcg ccc tac tac aag agg ctg ggc cgc gac gcg ctg ctc agc 816
821 Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser
822      260      265      270
824 tgg gac gac gtg ctg gcc gtg cag agc ctg tat ggg aag ccc cta ggg 864
825 Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly
826      275      280      285
828 ggc tca gtg gcc gtc cag ctc cca gga aag ctg ttc act gac ttt gag 912
829 Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu
830      290      295      300
832 acc tgg gac tcc tac agc ccc caa gga agg cgc cct gaa acg cag ggc 960
833 Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly
834 305      310      315      320
836 cct aaa tac tgc cac tct tcc ttc gat gcc atc act gta gac agg caa 1008
837 Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln
838      325      330      335
840 cag caa ctg tac att ttt aaa ggg agc cat ttc tgg gag gtg gca gct 1056
841 Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala
842      340      345      350
844 gat ggc aac gtc tca gag ccc cgt cca ctg cag gaa aga tgg gtc ggg 1104
845 Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly
846      355      360      365
848 ctg ccc ccc aac att gag gct gcg gca gtg tca ttg aat gat gga gat 1152

```

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```

849 Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser Leu Asn Asp Gly Asp
850      370      375      380
852 ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg ttc cgg ggc ccc aag 1200
853 Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys
854 385      390      395      400
856 cca gtg tgg ggt ctc cca cag ctg tgc cgg gca ggg ggc ctg ccc cgc 1248
857 Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg
858      405      410      415
860 cat cct gac gcc gcc ctc ttc ttc cct cct ctg cgc cgc ctc atc ctc 1296
861 His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu
862      420      425      430
864 ttc aag ggt gcc cgc tac tac gtg ctg gcc cga ggg gga ctg caa gtg 1344
865 Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Gly Leu Gln Val
866      435      440      445
868 gag ccc tac tac ccc cga agt ctg cag gac tgg gga ggc atc cct gag 1392
869 Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp Gly Gly Ile Pro Glu
870      450      455      460
872 gag gtc agc ggc gcc ctg ccg agg ccc gat ggc tcc atc atc ttc ttc 1440
873 Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe
874 465      470      475      480
876 cga gat gac cgc tac tgg cgc ctc gac cag gcc aaa ctg cag gca acc 1488
877 Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr
878      485      490      495
880 acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg atg ggc tgc tgg cat 1536
881 Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His
882      500      505      510
884 gcc aac tcg ggg agc gcc ctg ttc tga 1563
885 Ala Asn Ser Gly Ser Ala Leu Phe *
886      515      520

```

E--&gt; 888

- 7 -

-delete ✓

~~deleted~~

## VERIFICATION SUMMARY

DATE: 06/28/2002

PATENT APPLICATION: US/10/050,216A

TIME: 11:16:22

Input Set : A:\CORRECTEDSEQUENCE LISTING.txt

Output Set: N:\CRF3\06282002\J050216A.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:489 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:490 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!  
L:491 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:493 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:494 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!  
L:495 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:498 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:499 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!  
L:500 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:503 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:504 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!  
L:505 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:508 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0  
L:888 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:888 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1560 Found:1563 SEQ:10